

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: March 9, 2002, 00:48:45 ; Search time 2351.15 Seconds
(without alignments)
182.433 Million cell updates/sec

Title: US-09-851-670-18

Perfect score: 26

Sequence: 1 ttatgtggccatcttgcacat 26

Scoring table: IDENTITY_NUC

Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_rat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_om:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vl:*

Result No.	Score	Query Match Length	DB ID	Description
c 1	16.4	63.1	59 6 AX163544	I63544 Sequence 7
c 2	15.4	59.2	51 6 AX162579	AX162579 Sequence
c 3	15	57.7	50 6 AX162580	AX162580 Sequence
c 4	15	57.7	51 6 AX10915	AX10915 Sequence
c 5	14.6	56.2	36 6 AX136901	AR136901 Sequence
c 6	14.6	56.2	39 6 A08043	A08043 Oligonucleo
c 7	14.4	55.4	20 6 AX008459	AX008459 Sequence
c 8	14.2	54.6	39 6 AR151074	AR151074 Sequence
c 9	14.2	54.6	39 6 E15028	E15028 PCR primer
c 10	14.2	54.6	43 6 A67664	A67664 Sequence 84
c 11	14.2	54.6	43 6 AR089874	AR089874 Sequence
c 12	14.2	54.6	51 6 AX116937	AX116937 Sequence
c 13	14	53.8	27 6 E64521	E64521 Sugar-respo
c 14	14	53.8	40 6 AX055762	AX055762 Sequence
c 15	14	53.8	41 6 AR03976	AR03976 Sequence
c 16	14	53.8	51 6 AX167789	AX167789 Sequence
c 17	13.8	53.1	28 6 AX008017	AX008017 Sequence
c 18	13.8	53.1	45 6 F07961	E07961 Primer. 9/1
c 19	13.8	53.1	51 6 AX118393	AX118393 Sequence
c 20	13.6	52.3	37 6 AX097677	AX097677 Sequence
c 21	13.6	52.3	37 6 AX168879	AX168879 Sequence
c 22	13.6	52.3	37 6 AX167006	AX167006 Sequence
c 23	13.6	52.3	41 6 AR093977	AR093977 Sequence
c 24	13.4	51.5	51 6 AX157611	AX157611 Sequence
c 25	13.4	51.5	51 6 AX157612	AX157612 Sequence
c 26	13.4	51.5	51 6 AX165413	AX165413 Sequence
c 27	13.4	51.5	51 9 HSA93229	HSA93229 Homo sapi
c 28	13.4	51.5	58 6 AR095912	AR095912 Sequence
c 29	13.4	51.5	58 6 AR095913	AR095913 Sequence
c 30	13.2	50.8	18 6 AX165763	AX165763 Sequence
c 31	13.2	50.8	19 6 AR077976	AR077976 Sequence
c 32	13.2	50.8	27 6 A13225	A13225 Oligonucleo
c 33	13.2	50.8	27 6 AR034038	AR034038 Sequence
c 34	13.2	50.8	27 6 AR124047	AR124047 Sequence
c 35	13.2	50.8	31 6 AX077296	AX077296 Sequence
c 36	13.2	50.8	36 6 A08027	A08027 Oligonucleo
c 37	13.2	50.8	36 6 A13194	A13194 Oligonucleo
c 38	13.2	50.8	36 6 AR034033	AR034033 Sequence
c 39	13.2	50.8	36 6 AR034966	AR034966 Sequence
c 40	13.2	50.8	36 6 AR124042	AR124042 Sequence
c 41	13.2	50.8	39 22 E11772	E11772 Synthetic o
c 42	13.2	50.8	41 6 AX078135	AX078135 Sequence
c 43	13.2	50.8	41 6 AX078146	AX078146 Sequence
c 44	13.2	50.8	50 6 AX026789	AX026789 Sequence
c 45	13.2	50.8	51 6 AX161146	AX161146 Sequence

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8 SUMMARIES
BASE COUNT 22 a 14 c 15 g 8 t
ORIGIN

RESULT 14
AX055762/c
LOCUS AX055762 40 bp DNA
DEFINITION Sequence 77 from Patent WO0073348.
ACCESSION AX055762
VERSION AX055762.1 GI:12228874
KEYWORDS synthetic construct.
SOURCE
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 40)
AUTHORS Baker,R.P., Godard,A., Gurney,A.L., Hebert,C., Henzel,W.,
Kabakoff,R.C., Shelton,D.R., Smith,V., Watanabe,C.K. and Wood,W.I.
TITLE Methods and compositions for inhibiting neoplastic cell growth
JOURNAL Patent: WO 0073348-A 77 07-DEC-2000;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
SOURCE
/organism="synthetic construct"
/db_xref="Taxon:32630"
/note="Synthetic oligonucleotide probe."
BASE COUNT 10 a 9 c 12 g 9 t
ORIGIN

Query Match 53.8%; Score 14; DB 6; Length 40;
Best Local Similarity 77.3%; Pred. No. 5.1e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5 tggggccatcttggccaaat 26
||| |||| | ||||| |||||
Db 22 TGGGCCCCATCATCATTCCAGCAT 1

RESULT 15
AR093976/c
LOCUS AR093976 41 bp DNA
DEFINITION Sequence 14 from patent US 6001595.
ACCESSION AR093976
VERSION AR093976.1 GI:10020721
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS ilmen,M., Onnela,M. and Penttila ,M.
TITLE Promoters and uses thereof
JOURNAL Patent: US 6001595-A 14 14-DEC-1999;
FEATURES Location/Qualifiers
source
BASE COUNT 16 a 6 c 8 g 11 t
ORIGIN

Query Match 53.8%; Score 14; DB 6; Length 41;
Best Local Similarity 77.3%; Pred. No. 5.1e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ttatgtggccatctttttcca 22
||| ||| ||| ||||| |||
Db 25 TTATGAGCTATCTTATCGA 4

Search completed: March 9, 2002, 00:48:46
Job time: 11127 sec

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